

AMENDMENT TO THE SPECIFICATION

The last paragraph on page 4 and continuing on page 5 has been amended as follows:

Within the context of the present invention alignment are conveniently performed using BLAST, a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. Version BLAST 2.0 (Gapped BLAST) of this search tool has been made publicly available ~~on the internet~~ (currently retrievable from the Internet: <URL: <http://www.ncbi.nlm.nih.gov/BLAST/>>). It uses a heuristic algorithm which seeks local as opposed to global alignments and is therefore able to detect relationships among sequences which share only isolated regions. The scores assigned to a BLAST search have a well-defined statistical interpretation. Particularly useful within the score of the present invention are the blastp program allowing for the introduction of gaps in the local sequence alignments and the PSI-BLAST program, both programs comparing an amino acid query sequence against a protein sequence database, as well as a blastp variant program allowing local alignment of two sequences only. Said programs are preferably run with optional parameters set to the default values.

The third paragraph on page 5 has been amended as follows:

Sequence alignments using such computer programs reveal the presence of an ATP/GTP-binding motif A (amino acids 460 to 467 in SEQ ID NO: 3), the consensus sequence of which is (Ala/Gly)XaaXaaXaaXaaGlyLys(Ser/Thu) (SEQ ID NO: 34), wherein (Ala/Gly) indicates Ala or Gly, Xaa indicates any naturally occurring amino acid and (Ser/Thr) indicates Ser or Thr. Alignment additionally reveals a region (amino acid position 479 to 719 in SEQ ID NO: 3), similar to part to the ATPase/helicase domain of proteins in the SWI2/SNF2 family which are involved in chromatin remodeling but no significant overall sequence identity with known proteins.

Please insert the following Abstract on a separate page after the claims:

ABSTRACT

The present invention relates to DNA that encodes proteins involved in gene silencing. Related genes encoding proteins characterized by an amino acid sequence comprising a component sequence of at least 150 amino acid residues having 40% or more identity with an

aligned component sequence of SEQ ID NO 3 can be isolated from different sources such as mammalian or plant cells. Further disclosed is a method for isolating DNA according to the invention.

Please amend the specification by replacing the Sequence Listing with the Corrected Sequence Listing submitted herewith.